

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Stanley R. Krystek et al.
Serial No : Not yet known
Filed : May 10, 2001
For : MODIFIED INOSINE 5'-MONOPHOSPHATE
DEHYDROGENASE POLYPEPTIDES AND USES THEREOF

35 No. Arroyo Parkway
Pasadena, California 91103
May 10, 2001

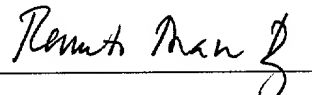
Assistant Commissioner for Patents
Box Sequence
Washington, D.C. 20231

SIR:

DECLARATION PURSUANT TO 37 C.F.R. §1.821(f)

I hereby declare that the content of the paper and computer readable copies of the Sequence Listings, submitted in the subject patent application in accordance with 37 C.F.R. §1.821(c) and (e), respectively, are the same.

Respectfully submitted,



Renato Marco P. Domingo

095918 051001
T00T50 8T6E9860

SEQUENCE LISTING

<110> Krystek, Stanley R.
 Sheriff, Steven
 Witmer, Mark R.
 Hollenbaugh, Diane L.
 Yan, Ning
 Mouravieff, Julie E.
 Einspahr, Howard M.
 Kish, Kevin

<120> MODIFIED INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE
 POLYPEPTIDES AND USES THEREOF

<130> DB24NP

<140> Not yet known
 <141> 2001-05-10

<150> 60/203,448
 <151> 2000-05-10

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<170> PatentIn Ver. 2.0

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30

Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln

35

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45

Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro

50

55

60

Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile

65

70

75

80

Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr

85

90

95

1. General Information	
1.1. Name of the project	1.2. Date of completion
1.3. Name of the client	1.4. Name of the contractor
1.5. Address of the client	1.6. Address of the contractor
1.7. Contact person	1.8. Contact person
1.9. Phone number	1.10. Fax number
1.11. E-mail address	1.12. Website
1.13. Project description	1.14. Project objectives
1.15. Project scope	1.16. Project budget
1.17. Project timeline	1.18. Project risks
1.19. Project status	1.20. Project conclusion
1.21. Project evaluation	1.22. Project recommendation
1.23. Project feedback	1.24. Project signature
1.25. Project approval	1.26. Project stamp
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1.37. Project server	1.38. Project client
1.39. Project user	1.40. Project administrator
1.41. Project manager	1.42. Project supervisor
1.43. Project coordinator	1.44. Project assistant
1.45. Project secretary	1.46. Project clerk
1.47. Project janitor	1.48. Project cleaner
1.49. Project gardener	1.50. Project painter
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Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
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Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
 20 25 30

Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35 40 45

Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50 55 60

Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
 65 70 75 80

Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95

Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Thr Pro
 100 105 110

Ile Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys Tyr
 115 120 125

Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp
 130 135 140

Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr Ile
 145 150 155 160

Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr
 165 170 175

Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg
180 185 190

Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala
195 200 205

Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr Ala
210 215 220

Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val
225 230 235 240

Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met
245 250 255

Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe
260 265 270

Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu Asp
275 280 285

Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala
290 295 300

Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys
305 310 315 320

Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln His
325 330 335

Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met
340 345 350

Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln
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Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe
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<210> 22
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<213> Homo sapiens

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Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
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Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
20 25 30

Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
35 40 45

Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
50 55 60

Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65 70 75 80

Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
85 90 95

Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Ser Pro
100 105 110

Ser Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys Tyr
115 120 125

Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp
130 135 140

Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr Ile
145 150 155 160

Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr
165 170 175

Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu Arg
180 185 190

Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala
195 200 205

Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr Ala
210 215 220

Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val
225 230 235 240

Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met

00150-05446

1997-98 Year of operation (n = 100)		1998-99 Year of operation (n = 100)		1999-00 Year of operation (n = 100)		2000-01 Year of operation (n = 100)	
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20-24	10	10	10	10	10	10	10
25-29	10	10	10	10	10	10	10
30-34	10	10	10	10	10	10	10
35-39	10	10	10	10	10	10	10
40-44	10	10	10	10	10	10	10
45-49	10	10	10	10	10	10	10
50-54	10	10	10	10	10	10	10
55-59	10	10	10	10	10	10	10
60-64	10	10	10	10	10	10	10
65-69	10	10	10	10	10	10	10
70-74	10	10	10	10	10	10	10
75-79	10	10	10	10	10	10	10
80-84	10	10	10	10	10	10	10
85-89	10	10	10	10	10	10	10
90-94	10	10	10	10	10	10	10
95-99	10	10	10	10	10	10	10
100-104	10	10	10	10	10	10	10
105-109	10	10	10	10	10	10	10
110-114	10	10	10	10	10	10	10
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Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35 40 45

Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50 55 60

Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
 65 70 75 80

Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95

Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Lys Pro
 100 105 110

Ile Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys Tyr
 115 120 125

Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp
 130 135 140

FOO"EEEO

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Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
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Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
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Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65 70 75 80

Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Ile Val
100 105 110

Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu Asp
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Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val Thr
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Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala
195 200 205

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Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala
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Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys
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Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln His
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Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met
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Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln
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Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
35 40 45

Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
50 55 60

Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65 70 75 80

Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
85 90 95

Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Ser Pro
100 105 110

100150"BT6E960

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Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys	Tyr	Ile	145	150	155
Lys	Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	Val	Thr	165	170	175
Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala	Leu	Arg	180	185	190
Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	Leu	Ala	195	200	205
Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu	Tyr	Ala	210	215	220
Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln	Asn	Val	225	230	235
Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	Met	Met	245	250	255
Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	Phe	Phe	260	265	270
Ser	Asp	Gly	Ile	Arg	Leu	Lys	Lys	Tyr	Arg	Gly	Met	Gly	Ser	Leu	Asp	275	280	285
Ala	Met	Asp	Lys	His	Leu	Ser	Ser	Gln	Asn	Arg	Tyr	Phe	Ser	Glu	Ala	290	295	300
Asp	Lys	Ile	Lys	Val	Ala	Gln	Gly	Val	Ser	Gly	Ala	Val	Gln	Asp	Lys	305	310	315
Gly	Ser	Ile	His	Lys	Phe	Val	Pro	Tyr	Leu	Ile	Ala	Gly	Ile	Gln	His	325	330	335
Ser	Cys	Gln	Asp	Ile	Gly	Ala	Lys	Ser	Leu	Thr	Gln	Val	Arg	Ala	Met	340	345	350
Met	Tyr	Ser	Gly	Glu	Leu	Lys	Phe	Glu	Lys	Arg	Thr	Ser	Ser	Ala	Gln	355	360	365

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Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu Ala		
195	200	205
Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr Ala		
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Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn Val		
225	230	235
Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met Met		
245	250	255
Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe Phe		
260	265	270
Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu Asp		
275	280	285
Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu Ala		
290	295	300
Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp Lys		
305	310	315
Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln His		
325	330	335
Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala Met		
340	345	350
Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala Gln		
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Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu Phe		
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Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
 20 25 30

Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
 35 40 45

Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
 50 55 60

Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
 65 70 75 80

Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95

Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Gln Pro
 100 105 110

Gln Ser Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys
 115 120 125

Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu
 130 135 140

Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr
 145 150 155 160

Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val
 165 170 175

Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu
 180 185 190

Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu
 195 200 205

Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr
 210 215 220

TCF30" 8T6E3860

Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp
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Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln
325 330 335

His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala
340 345 350

Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala
355 360 365

Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu
370 375 380

Phe
385

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Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
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Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
20 25 30

Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
35 40 45

Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
50 55 60

Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65 70 75 80

Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
85 90 95

Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Ser Pro
100 105 110

Thr Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys

Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu
 130 135 140
 Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr
 145 150 155 160
 Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val
 165 170 175
 Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu
 180 185 190
 Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu
 195 200 205
 Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr
 210 215 220
 Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn
 225 230 235 240
 Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met
 245 250 255
 Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe
 260 265 270
 Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu
 275 280 285
 Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu
 290 295 300
 Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp
 305 310 315 320
 Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln
 325 330 335
 His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala
 340 345 350
 Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala
 355 360 365
 Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu

380

Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu
180 185 190

Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu
195 200 205

Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr
210 215 220

Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn
225 230 235 240

Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met
245 250 255

Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe
260 265 270

Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu
275 280 285

Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu
290 295 300

Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp
305 310 315 320

Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln
325 330 335

His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala
340 345 350

Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala
355 360 365

Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu
370 375 380

Phe
385

<210> 36

<211> 385

<212> PRT

<213> Homo sapiens

<400> 36

Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
1 5 10 15

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Gly	Leu	Thr	Ala	Gln	Gln	Leu	Phe	Asn	Cys	Gly	Asp	Gly	Leu	Thr	Tyr	20	25	30	
Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Tyr	Ile	Asp	Phe	Thr	Ala	Asp	Gln	35	40	45	
Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys	Thr	Pro	50	55	60	
Leu	Val	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	Ala	Ile	65	70	75	80
Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr	85	90	95	
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Ala	Gly	100	105	110	
Arg	Pro	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp	Lys	115	120	125	
Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val	Leu	130	135	140	
Asp	Ser	Ser	Gln	Gly	Asn	Ser	Ile	Phe	Gln	Ile	Asn	Met	Ile	Lys	Tyr	145	150	155	160
Ile	Lys	Asp	Lys	Tyr	Pro	Asn	Leu	Gln	Val	Ile	Gly	Gly	Asn	Val	Val	165	170	175	
Thr	Ala	Ala	Gln	Ala	Lys	Asn	Leu	Ile	Asp	Ala	Gly	Val	Asp	Ala	Leu	180	185	190	
Arg	Val	Gly	Met	Gly	Ser	Gly	Ser	Ile	Cys	Ile	Thr	Gln	Glu	Val	Leu	195	200	205	
Ala	Cys	Gly	Arg	Pro	Gln	Ala	Thr	Ala	Val	Tyr	Lys	Val	Ser	Glu	Tyr	210	215	220	
Ala	Arg	Arg	Phe	Gly	Val	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Gln	Asn	225	230	235	240
Val	Gly	His	Ile	Ala	Lys	Ala	Leu	Ala	Leu	Gly	Ala	Ser	Thr	Val	Met	245	250	255	
Met	Gly	Ser	Leu	Leu	Ala	Ala	Thr	Thr	Glu	Ala	Pro	Gly	Glu	Tyr	Phe	260	265	270	

95

His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala

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340

345

350

Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala
355 360 365

Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu
370 375 380

Phe
385

<210> 38

<211> 385

<212> PRT

<213> Homo sapiens

<400> 38

Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
1 5 10 15

Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
20 25 30

Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
35 40 45

Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
50 55 60

Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65 70 75 80

Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
85 90 95

Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Asn Ser
100 105 110

Pro Leu Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys
115 120 125

Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu
130 135 140

Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr
145 150 155 160

<212> PRT

<213> Homo sapiens

<400> 39

Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Ser Tyr Val Pro Asp Asp
1 5 10 15

Gly Leu Thr Ala Gln Gln Leu Phe Asn Cys Gly Asp Gly Leu Thr Tyr
20 25 30

Asn Asp Phe Leu Ile Leu Pro Gly Tyr Ile Asp Phe Thr Ala Asp Gln
35 40 45

Val Asp Leu Thr Ser Ala Leu Thr Lys Lys Ile Thr Leu Lys Thr Pro
50 55 60

Leu Val Ser Ser Pro Met Asp Thr Val Thr Glu Ala Gly Met Ala Ile
65 70 75 80

Ala Met Ala Leu Thr Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
85 90 95

Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Tyr Tyr Gly
100 105 110

Thr Trp Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp Lys
115 120 125

Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val Leu
130 135 140

Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys Tyr
145 150 155 160

Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val Val
165 170 175

Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala Leu
180 185 190

Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val Leu
195 200 205

Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu Tyr
210 215 220

Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln Asn
225 230 235 240

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Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val Met
245 250 255

Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr Phe
260 265 270

Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser Leu
275 280 285

Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser Glu
290 295 300

Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln Asp
305 310 315 320

Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile Gln
325 330 335

His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg Ala
340 345 350

Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser Ala
355 360 365

Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg Leu
370 375 380

Phe
385

<210> 40

<211> 1155

<212> DNA

<213> Homo sapiens

<400> 40

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cagcagctct tcaactgcgg agaaggcctc acctacaatg actttctcat tctccctggg 120
tacatcgact tcaactgcga ccagggtggac ctgacttctg ctctgaccaa gaaaatcact 180
cttaagaccc cactggtttc ctctcccatg gacacagtca cagaggctgg gatggccata 240
gcaatggcgc ttacaggcgg tattggcttc atccaccaca actgtacacc tgaattccag 300
gccaatgaag ttcggaaagt gaagaaatat gacaagaccc tgctgtgtgg ggcagccatt 360
ggcactcatg aggatgacaa gtataggctg gacttgctcg cccaggctgg tgtggatgta 420
gtgggttttg actcttccca gggaaattcc atcttccaga tcaatatgat caagtacatc 480
aaagacaaat accctaattc ccaagtcatt ggaggcaatg tggtaactgc tgcccaggcc 540
aagaacctca ttgatgcagg tgtggatgcc ctgcgggtgg gcatgggaag tggctccatc 600

[illegible]

<400> 41

<210> 42

<212> DNA

<400> 42

40

Table 1. Demographic characteristics of the study population	
Age (years)	65.0 ± 1.5
Gender	
Male	50 (50.0%)
Female	50 (50.0%)
Education (years)	12.0 ± 1.0
Marital status	
Married	40 (80.0%)
Single	10 (20.0%)
Occupation	
Retired	40 (80.0%)
Unemployed	10 (20.0%)
Income (USD/month)	1,200 ± 200
Health status	
Good	30 (60.0%)
Fair	20 (40.0%)
Poor	10 (20.0%)
Comorbidities	
Hypertension	20 (40.0%)
Diabetes	10 (20.0%)
Cholesterol	15 (30.0%)
Smoking status	
Smoker	10 (20.0%)
Non-smoker	40 (80.0%)
Alcohol consumption	
Regular	5 (10.0%)
Occasional	15 (30.0%)
Never	30 (60.0%)

<211> 1155

<213> Homo sapiens

atggcgcact	acctgattag	tgggggcacg	tctacgtgc	cagacgacgg	actcacagca	60
cagcagctct	tcaactggcg	agacggcctc	acctacaatg	actttctcat	tctccctggg	120
tacatcgact	tactgcaga	ccaggtggac	ctgacttctg	ctctgaccaa	gaaaatcact	180
cttaagaccc	cactggtttc	ctctcccatg	gacacagtca	cagaggctgg	gatggccata	240
gcaatggcgc	ttacaggcgg	tattggcttc	atccaccaca	actgtacacc	tgaattccag	300
gccaatgaag	ttcggaaagt	gaagaaatat	tctccgactc	tgtctgtgtg	ggcagccatt	360
ggcactcatg	aggatgacaa	gtataggctg	gacttgctcg	cccaggctgg	tgtggatgta	420
gtgggttttg	actcttccca	gggaaattcc	atcttccaga	tcaatatgat	caagtacatc	480
aaagacaaat	accctaattc	ccaagtcatt	ggaggcaatg	tggtcactgc	tgcccaggcc	540
aagaacctca	ttgatgcagg	tgtggatgcc	ctgcgggttg	gcatgggaag	tggctccatc	600
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ggtcataattg	cgaaagcctt	ggcccttggg	gcctccacag	tcatgatggg	ctctctcctg	780
gctgccacca	ctgaggcccc	tgggtgaatac	ttcttttccg	atgggataccg	gctaaagaaa	840
tatcgcggtg	tgggttctct	cgatgccatg	gacaagcacc	tcagcagcca	gaacagatat	900
ttcagtgaag	ctgacaaaat	caaagtggcc	cagggagtgt	ctgggtgctgt	gcaggacaaa	960
gggtcaatcc	acaaatttgt	cccttacctg	attgctggca	tccaacactc	atgccaggac	1020
attgggtgcca	agagcttgac	ccaagtccga	gccatgatgt	actctgggga	gcttaagttt	1080
gagaagagaa	cgtcctcagc	ccaggtggaa	ggtggcgctc	atagcctcca	ttcgtatgag	1140
aaqcgqcttt	tctga					1155

<211> 1155

<213> Homo sapiens

<400> 44

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ttcatagact	tcatagctga	tgaggtggac	ctgacctcag	ccctgaccgg	gaagatcacg	180
ctgaagacgc	cactgatctc	ctcccccatg	gacactgtga	cagaggctga	catggccatt	240
gccatggctc	tgatgggagg	tattgggtttc	attcaccaca	actgcacccc	agagttccag	300
gccaacgagg	tgcggaaggt	caagaagttt	gacaaaaccc	tgctctgtgg	ggcagctgtg	360
ggcaccgctg	aggatgacaa	ataccgtctg	gacctgctca	cccaggcggg	cgtcgacgtc	420
atagtcttgg	actcgtccca	agggaattcg	gtgtatcaaa	tcgccatggt	gcattacatc	480
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ggacacgtgg	tcaaggccct	ggcccttggg	gcctccacag	tgatgatggg	ctccctgctg	780
gccgccacta	cggaggcccc	tggcgagtac	ttcttctcag	acgggggtgcg	gctcaagaag	840
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ttcagcgagg	gggataaaagt	gaagatcgcg	cagggtgtct	cgggctccat	ccaggacaaa	960
ggatccattc	agaagttcgt	gccctacctc	atagcaggca	tccaacacgg	ctgccaggat	1020
atcggggccc	gcagcctgtc	tgtccttcgg	tccatgatgt	actcaggaga	gctcaagttt	1080
gagaagcgga	ccatgtcggc	ccagattgag	ggtggtgtcc	atggcctgca	ctcttacgaa	1140
aagcggtgtg	actga					1155

<210> 45

<211> 1158

<212> DNA

<213> Homo sapiens

<400> 45

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cagcagctct	tcaactgcgg	agacggcctc	acctacaatg	actttctcat	tctccctggg	120
tacatcgact	tactgcaga	ccagggtggac	ctgacttctg	ctctgaccaa	gaaaatcact	180
cttaagaccc	cactggtttc	ctctcccatg	gacacagtca	cagaggctgg	gatggccata	240
gcaatggcgc	ttacaggcgg	tattggcttc	atccaccaca	actgtacacc	tgaattccag	300
gccaatgaag	ttcggaaagt	gaagaaatat	tctccgactc	agctgctgtg	tggggcagcc	360
attggcactc	atgaggatga	caagtatagg	ctggacttgc	tcgccagggc	tggtgtggat	420
gtagtggttt	tggactcttc	ccagggaaat	tccatcttcc	agatcaatat	gatcaagtac	480
atcaaagaca	aataccctaa	tctccaagtc	attggaggca	atgtggtcac	tgctgccag	540
gccagaacc	tcattgatgc	aggtgtggat	gccctgcggg	tgggcatggg	aagtggctcc	600
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gtgtcagagt	atgcacggcg	ctttggtgtt	ccggtcattg	ctgatggagg	aatccaaaat	720
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aaatatcgcg	gtatgggttc	tctcgatgcc	atggacaagc	acctcagcag	ccagaacaga	900
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gacattggtg	ccaagagctt	gacccaagtc	cgagccatga	tgtactctgg	ggagcttaag	1080
tttgagaaga	gaacgtcctc	agcccagggtg	gaagggtggcg	tccatagcct	ccattcgtat	1140

1158

<211> 1158

<212> DNA

<213> Homo sapiens

<400> 46

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cagcagctct	tcaactgcgg	agacggcctc	acctacaatg	actttctcat	tctcctggg	120
tacatcgact	tcactgcaga	ccaggtggac	ctgacttctg	ctctgaccaa	gaaaatcact	180
cttaagaccc	cactggtttc	ctctcccatt	gacacagtca	cagaggctgg	gatggccata	240
gcaatggcgc	ttacaggcgg	tattggcttc	atccaccaca	actgtacacc	tgaattccag	300
gccaatgaag	ttcggaagt	gaagaaatat	gctggctgct	cgctgctgtg	tggggcagcc	360
attggcactc	atgaggatga	caagtatagg	ctggacttgc	tcgccaggc	tgggtgtgat	420
gtagtggttt	tggactcttc	ccagggaat	tccatcttcc	agatcaatat	gatcaagtac	480
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gtgtcagagt	atgcacggcg	ctttgggtgt	ccggctcatt	ctgatggagg	aatccaaaat	720
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ctggctgcca	ccactgaggc	ccctggtgaa	tacttctttt	ccgatgggat	ccggctaaag	840
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gacattggtg	ccaagagctt	gacccaagtc	cgagccatga	tgtactctgg	ggagcttaag	1080
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gagaagcggc	ttttctga					1158

<210> 47

<211> 1158

<212> DNA

<213> Homo sapiens

<400> 47

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tacatcgact	tcaactgcaga	ccagggtggac	ctgacttctg	ctctgaccaa	gaaaatcaact	180
cttaagaccc	cactggtttc	ctctcccatg	gacacagtca	cagaggctgg	gatggccata	240
gcaatggcgc	ttacaggcgg	tattggcttc	atccaccaca	actgtacacc	tgaattccag	300
gccaatgaag	ttcggaagt	gaagaaatat	aactctccgc	ttctgctgtg	tggggcagcc	360
attggcactc	atgaggatga	caagtatagg	ctggacttgc	tcgcccaggc	tgggtgtggat	420
gtagtggttt	tggactcttc	ccagggaagt	tccatcttcc	agatcaatat	gatcaagtac	480
atcaaagaca	aataccctaa	tctccaagtc	attggaggca	atgtggtcac	tgctgccag	540
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gtgtcagagt	atgcacggcg	ctttggtgtt	ccggtcattg	ctgatggagg	aatccaaaat	720
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 tttgagaaga gaacgtcctc agcccaggtg gaaggtggcg tccatagcct ccattcgtat 1140
 gagaagcggc ttttctga 1158

<210> 48

<211> 514

<212> PRT

<213> Homo sapiens

<400> 48

Met Ala Asp Tyr Leu Ile Ser Gly Gly Thr Gly Tyr Val Pro Glu Asp
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Gly Leu Thr Ala Gln Gln Leu Phe Ala Ser Ala Asp Asp Leu Thr Tyr
 20 25 30

Asn Asp Phe Leu Ile Leu Pro Gly Phe Ile Asp Phe Ile Ala Asp Glu
 35 40 45

Val Asp Leu Thr Ser Ala Leu Thr Arg Lys Ile Thr Leu Lys Thr Pro
 50 55 60

Leu Ile Ser Ser Pro Met Asp Thr Val Thr Glu Ala Asp Met Ala Ile
 65 70 75 80

Ala Met Ala Leu Met Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95

Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Asn Phe Glu Gln
 100 105 110

Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Ser His Thr Val Gly
 115 120 125

Asp Val Leu Glu Ala Lys Met Arg His Gly Phe Ser Gly Ile Pro Ile
 130 135 140

Thr Glu Thr Gly Thr Met Gly Ser Lys Leu Val Gly Ile Val Thr Ser
 145 150 155 160

Arg Asp Ile Asp Phe Leu Ala Glu Lys Asp His Thr Thr Leu Leu Ser
 165 170 175

Glu Val Met Thr Pro Arg Ile Glu Leu Val Val Ala Pro Ala Gly Val

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180	185	190
Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys		
195	200	205
Leu Pro Ile Val Asn Asp Cys Asp Glu Leu Val Ala Ile Ile Ala Arg		
210	215	220
Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ser		
225	230	235 240
Gln Lys Gln Leu Leu Cys Gly Ala Ala Val Gly Thr Arg Glu Asp Asp		
245	250	255
Lys Tyr Arg Leu Asp Leu Leu Thr Gln Ala Gly Val Asp Val Ile Val		
260	265	270
Leu Asp Ser Ser Gln Gly Asn Ser Val Tyr Gln Ile Ala Met Val His		
275	280	285
Tyr Ile Lys Gln Lys Tyr Pro His Leu Gln Val Ile Gly Gly Asn Val		
290	295	300
Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Gly		
305	310	315 320
Leu Arg Val Gly Met Gly Cys Gly Ser Ile Cys Ile Thr Gln Glu Val		
325	330	335
Met Ala Cys Gly Arg Pro Gln Gly Thr Ala Val Tyr Lys Val Ala Glu		
340	345	350
Tyr Ala Arg Arg Phe Gly Val Pro Ile Ile Ala Asp Gly Gly Ile Gln		
355	360	365
Thr Val Gly His Val Val Lys Ala Leu Ala Leu Gly Ala Ser Thr Val		
370	375	380
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr		
385	390	395 400
Phe Phe Ser Asp Gly Val Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser		
405	410	415
Leu Asp Ala Met Glu Lys Ser Ser Ser Ser Gln Lys Arg Tyr Phe Ser		
420	425	430
Glu Gly Asp Lys Val Lys Ile Ala Gln Gly Val Ser Gly Ser Ile Gln		

[illegible][illegible]

Asp Val Phe Glu Ala Lys Ala Arg His Gly Phe Cys Gly Ile Pro Ile
 130 135 140
 Thr Asp Thr Gly Arg Met Gly Ser Arg Leu Val Gly Ile Ile Ser Ser
 145 150 155 160
 Arg Asp Ile Asp Phe Leu Lys Glu Glu Glu His Asp Cys Phe Leu Glu
 165 170 175
 Glu Ile Met Thr Lys Arg Glu Asp Leu Val Val Ala Pro Ala Gly Ile
 180 185 190
 Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
 195 200 205
 Leu Pro Ile Val Asn Glu Asp Asp Glu Leu Val Ala Ile Ile Ala Arg
 210 215 220
 Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ala
 225 230 235 240
 Lys Lys Gln Leu Leu Cys Gly Ala Ala Ile Gly Thr His Glu Asp Asp
 245 250 255
 Lys Tyr Arg Leu Asp Leu Leu Ala Gln Ala Gly Val Asp Val Val Val
 260 265 270
 Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
 275 280 285
 Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
 290 295 300
 Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
 305 310 315 320
 Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val
 325 330 335
 Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
 340 345 350
 Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
 355 360 365
 Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
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Val Gly Asp Val Leu Glu Ala Lys Met Arg His Gly Phe Ser Gly Ile
20 25 30
Pro Ile Thr Glu Thr Gly Thr Met Gly Ser Lys Leu Val Gly Ile Val
35 40 45
Thr Ser Arg Asp Ile Asp Phe Leu Ala Glu Lys Asp His Thr Thr Leu
50 55 60
Leu Ser Glu Val Met Thr Pro Arg Ile Glu Leu Val Val Ala Pro Ala
65 70 75 80
Gly Val Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys
85 90 95
Gly Lys Leu Pro Ile Val Asn Asp Cys Asp Glu Leu Val Ala Ile Ile
100 105 110
Ala Arg Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys

125

Asp Val Leu Glu Ala Lys Met Arg His Gly Phe Ser Gly Ile Pro Ile
130 135 140

Thr Glu Thr Gly Thr Met Gly Ser Lys Leu Val Gly Ile Val Thr Ser
145 150 155 160

Arg Asp Ile Asp Phe Leu Ala Glu Lys Asp His Thr Thr Leu Leu Ser
165 170 175

Glu Val Met Thr Pro Arg Ile Glu Leu Val Val Ala Pro Ala Gly Val
180 185 190

Thr Leu Lys Glu Ala Asn Glu Ile Leu Gln Arg Ser Lys Lys Gly Lys
195 200 205

Leu Pro Ile Val Asn Asp Cys Asp Glu Leu Val Ala Ile Ile Ala Arg
210 215 220

Thr Asp Leu Lys Lys Asn Arg Asp Tyr Pro Leu Ala Ser Lys Asp Ser
225 230 235 240

Gln Lys Gln Leu Leu Cys Gly Ala Ala Val Gly Thr Arg Glu Asp Asp
245 250 255

Lys Tyr Arg Leu Asp Leu Leu Thr Gln Ala Gly Val Asp Val Ile Val
260 265 270

Leu Asp Ser Ser Gln Gly Asn Ser Val Tyr Gln Ile Ala Met Val His
275 280 285

Tyr Ile Lys Gln Lys Tyr Pro His Leu Gln Val Ile Gly Gly Asn Val
290 295 300

Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Gly
305 310 315 320

Leu Arg Val Gly Met Gly Cys Gly Ser Ile Cys Ile Thr Gln Glu Val
325 330 335

Met Ala Cys Gly Arg Pro Gln Gly Thr Ala Val Tyr Lys Val Ala Glu
340 345 350

Tyr Ala Arg Arg Phe Gly Val Pro Ile Ile Ala Asp Gly Gly Ile Gln
355 360 365

Thr Val Gly His Val Val Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
370 375 380

Gly	Leu	Thr	Ala	Gln	Gln	Leu	Phe	Asn	Cys	Gly	Asp	Gly	Leu	Thr	Tyr			
			20						25					30				
Asn	Asp	Phe	Leu	Ile	Leu	Pro	Gly	Tyr	Ile	Asp	Phe	Thr	Ala	Asp	Gln			
		35					40					45						
Val	Asp	Leu	Thr	Ser	Ala	Leu	Thr	Lys	Lys	Ile	Thr	Leu	Lys	Thr	Pro			
		50					55					60						
Leu	Val	Ser	Ser	Pro	Met	Asp	Thr	Val	Thr	Glu	Ala	Gly	Met	Ala	Ile			
		65				70				75					80			
Ala	Met	Ala	Leu	Thr	Gly	Gly	Ile	Gly	Phe	Ile	His	His	Asn	Cys	Thr			
				85					90						95			
Pro	Glu	Phe	Gln	Ala	Asn	Glu	Val	Arg	Lys	Val	Lys	Lys	Tyr	Glu	Gln			
			100					105						110				
Gly	Phe	Ile	Thr	Asp	Pro	Val	Val	Leu	Ser	Pro	Lys	Asp	Arg	Val	Arg			
		115					120					125						
Asp	Val	Phe	Glu	Ala	Lys	Ala	Arg	His	Gly	Phe	Cys	Gly	Ile	Pro	Ile			
		130					135				140							
Thr	Asp	Thr	Gly	Arg	Met	Gly	Ser	Arg	Leu	Val	Gly	Ile	Ile	Ser	Ser			
		145				150				155					160			
Arg	Asp	Ile	Asp	Phe	Leu	Lys	Glu	Glu	Glu	His	Asp	Cys	Phe	Leu	Glu			
				165				170						175				
Glu	Ile	Met	Thr	Lys	Arg	Glu	Asp	Leu	Val	Val	Ala	Pro	Arg	Ser	Ile			
			180					185					190					
Thr	Leu	Lys	Glu	Ala	Asn	Glu	Ile	Leu	Gln	Arg	Ser	Lys	Lys	Gly	Lys			
		195						200				205						
Leu	Pro	Ile	Val	Asn	Glu	Asp	Asp	Glu	Leu	Val	Ala	Ile	Ile	Ala	Arg			
		210					215					220						
Thr	Asp	Leu	Lys	Lys	Asn	Arg	Asp	Tyr	Pro	Leu	Ala	Ser	Lys	Asp	Ala			
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Lys	Lys	Gln	Leu	Leu	Cys	Gly	Ala	Ala	Ile	Gly	Thr	His	Glu	Asp	Asp			
			245						250					255				
Lys	Tyr	Arg	Leu	Asp	Leu	Leu	Ala	Gln	Ala	Gly	Val	Asp	Val	Val	Val			
			260					265					270					

Leu Asp Ser Ser Gln Gly Asn Ser Ile Phe Gln Ile Asn Met Ile Lys
 275 280 285

Tyr Ile Lys Asp Lys Tyr Pro Asn Leu Gln Val Ile Gly Gly Asn Val
 290 295 300

Val Thr Ala Ala Gln Ala Lys Asn Leu Ile Asp Ala Gly Val Asp Ala
 305 310 315 320

Leu Arg Val Gly Met Gly Ser Gly Ser Ile Cys Ile Thr Gln Glu Val
 325 330 335

Leu Ala Cys Gly Arg Pro Gln Ala Thr Ala Val Tyr Lys Val Ser Glu
 340 345 350

Tyr Ala Arg Arg Phe Gly Val Pro Val Ile Ala Asp Gly Gly Ile Gln
 355 360 365

Asn Val Gly His Ile Ala Lys Ala Leu Ala Leu Gly Ala Ser Thr Val
 370 375 380

Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr
 385 390 395 400

Phe Phe Ser Asp Gly Ile Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser
 405 410 415

Leu Asp Ala Met Asp Lys His Leu Ser Ser Gln Asn Arg Tyr Phe Ser
 420 425 430

Glu Ala Asp Lys Ile Lys Val Ala Gln Gly Val Ser Gly Ala Val Gln
 435 440 445

Asp Lys Gly Ser Ile His Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile
 450 455 460

Gln His Ser Cys Gln Asp Ile Gly Ala Lys Ser Leu Thr Gln Val Arg
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Ala Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Ser Ser
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Ala Gln Val Glu Gly Gly Val His Ser Leu His Ser Tyr Glu Lys Arg
 500 505 510

Leu Phe

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<301> Dayton, Jennifer S.
 Lindsten, Tullia
 Thompson, Craig B.
 Mitchell, Beverly S.

<302> Effects of Human T Lymphocyte Activation on Inosine
 Monophosphate Dehydrogenase Expression

<303> J. Immunol.

<304> 152

<306> 984-991

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Gly Leu Thr Ala His Glu Leu Phe Ala Ser Ala Asp Gly Leu Thr Tyr
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Asn Asp Phe Leu Ile Leu Pro Gly Phe Ile Asp Phe Ile Ala Asp Glu
 35 40 45

Val Asp Leu Thr Ser Ala Leu Thr Arg Lys Ile Thr Leu Lys Thr Pro
 50 55 60

Leu Ile Ser Ser Pro Met Asp Thr Val Thr Glu Ala Asp Met Ala Ile
 65 70 75 80

Ala Met Ala Leu Met Gly Gly Ile Gly Phe Ile His His Asn Cys Thr
 85 90 95

Pro Glu Phe Gln Ala Asn Glu Val Arg Lys Val Lys Lys Phe Glu Gln
 100 105 110

Gly Phe Ile Thr Asp Pro Val Val Leu Ser Pro Ser His Thr Val Gly
 115 120 125

Asp Val Leu Glu Ala Lys Met Arg His Gly Phe Ser Gly Ile Pro Ile
 130 135 140

Thr Glu Thr Gly Thr Met Gly Ser Lys Leu Val Gly Ile Val Thr Ser
 145 150 155 160

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	325		330		335	
Met Ala Cys Gly Arg Pro Gln Gly Thr Ala Val Tyr Lys Val Ala Glu						
	340		345		350	
Tyr Ala Arg Arg Phe Gly Val Pro Ile Ile Ala Asp Gly Gly Ile Gln						
	355		360		365	
Thr Val Gly His Val Val Lys Ala Leu Ala Leu Gly Ala Ser Thr Val						
	370		375		380	
Met Met Gly Ser Leu Leu Ala Ala Thr Thr Glu Ala Pro Gly Glu Tyr						
385		390		395		400
Phe Phe Ser Asp Gly Val Arg Leu Lys Lys Tyr Arg Gly Met Gly Ser						
	405		410		415	
Leu Asp Pro Met Glu Lys Ser Ser Ser Ser Gln Lys Arg Tyr Phe Ser						
	420		425		430	
Glu Gly Asp Lys Val Lys Ile Ala Gln Gly Val Ser Gly Ser Ile Gln						
	435		440		445	
Asp Lys Gly Ser Ile Gln Lys Phe Val Pro Tyr Leu Ile Ala Gly Ile						
	450		455		460	
Gln His Gly Cys Gln Asp Ile Gly Ala Arg Ser Leu Ser Val Leu Arg						
465		470		475		480
Ser Met Met Tyr Ser Gly Glu Leu Lys Phe Glu Lys Arg Thr Met Ser						
	485		490		495	
Pro Gln Ile Glu Gly Gly Val His Gly Leu His Ser Tyr Glu Lys Arg						
	500		505		510	
Leu Tyr						